



## SEQUENCE LISTING

Selden, Richard F.  
Miller, Allan M.  
Treco, Douglas A.

<120> OPTIMIZED MESSENGER RNA

<130> 10278-009001

<140> US 09/407,605

<141> 1999-09-28

<150> US 60/130,241

<151> 1999-04-20

<150> 60/102,239

<151> 1998-09-29

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Cys	Leu	Leu	Arg	Phe	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	
			15					20					25			

gcc	gtg	gag	ctg	agc	tgg	gac	tac	atg	cag	agc	gac	ctg	ggc	gag	ctg	147
Ala	Val	Glu	Leu	Ser	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	
			30				35						40			

ccc	gtg	gac	gcc	cgc	ttc	ccc	ccc	cgc	gtg	ccc	aag	agc	ttc	ccc	ttc	195
Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	
		45					50				55					

aac	acc	agc	gtg	gtg	tac	aag	aag	acc	ctg	ttc	gtg	gag	ttc	acc	gac	243
Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	
		60				65				70					75	

cac	ctg	ttc	aac	atc	gcc	aag	ccc	cgc	ccc	ccc	tgg	atg	ggc	ctg	ctg	291
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His	Leu	Phe	Asn	Ile	Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu		
				80					85					90			
ggc	ccc	acc	atc	cag	gcc	gag	gtg	tac	gac	acc	gtg	gtg	atc	acc	ctg	339	
Gly	Pro	Thr	Ile	Gln	Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu		
			95					100					105				
aag	aac	atg	gcc	agc	cac	ccc	gtg	agc	ctg	cac	gcc	gtg	ggc	gtg	agc	387	
Lys	Asn	Met	Ala	Ser	His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser		
		110					115					120					
tac	tgg	aag	gcc	agc	gag	ggc	gcc	gag	tac	gac	gac	cag	acc	agc	cag	435	
Tyr	Trp	Lys	Ala	Ser	Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln		
	125					130					135						
cgc	gag	aag	gag	gac	gac	aag	gtg	ttc	ccc	ggc	ggc	agc	cac	acc	tac	483	
Arg	Glu	Lys	Glu	Asp	Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr		
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gtg	tgg	cag	gtg	ctg	aag	gag	aac	ggc	ccc	atg	gcc	agc	gac	ccc	ctg	531	
Val	Trp	Gln	Val	Leu	Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu		
				160					165					170			
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Cys	Leu	Thr	Tyr	Ser	Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu		
			175					180					185				
aac	agc	ggc	ctg	atc	ggc	gcc	ctg	ctg	gtg	tgc	cgc	gag	ggc	agc	ctg	627	
Asn	Ser	Gly	Leu	Ile	Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu		
		190					195					200					
gcc	aag	gag	aag	acc	cag	acc	ctg	cac	aag	ttc	atc	ctg	ctg	ttc	gcc	675	
Ala	Lys	Glu	Lys	Thr	Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala		
	205					210					215						
gtg	ttc	gac	gag	ggc	aag	agc	tgg	cac	agc	gag	acc	aag	aac	agc	ctg	723	
Val	Phe	Asp	Glu	Gly	Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu		
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Met	Gln	Asp	Arg	Asp	Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His		
				240					245					250			
acc	gtg	aac	ggc	tac	gtg	aac	cgc	agc	ctg	ccc	ggc	ctg	atc	ggc	tgc	819	
Thr	Val	Asn	Gly	Tyr	Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys		
			255					260					265				
cac	cgc	aag	agc	gtg	tac	tgg	cac	gtg	atc	ggc	atg	ggc	acc	acc	ccc	867	
His	Arg	Lys	Ser	Val	Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro		
		270					275					280					
gag	gtg	cac	agc	atc	ttc	ctg	gag	ggc	cac	acc	ttc	ctg	gtg	cgc	aac	915	
Glu	Val	His	Ser	Ile	Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn		
	285					290					295						
cac	cgc	cag	gcc	agc	ctg	gag	atc	agc	ccc	atc	acc	ttc	ctg	acc	gcc	963	
His	Arg	Gln	Ala	Ser	Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala		

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cag acc ctg ctg atg gac ctg ggc cag ttc ctg ctg ttc tgc cac atc				1011
Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile				
320		325	330	
agc agc cac cag cac gac ggc atg gag gcc tac gtg aag gtg gac agc				1059
Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser				
335		340	345	
tgc ccc gag gag ccc cag ctg cgc atg aag aac aac gag gag gcc gag				1107
Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu				
350		355	360	
gac tac gac gac gac ctg acc gac agc gag atg gac gtg gtg cgc ttc				1155
Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe				
365		370	375	
gac gac gac aac agc ccc agc ttc atc cag atc cgc agc gtg gcc aag				1203
Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys				
380		385	390	395
aag cac ccc aag acc tgg gtg cac tac atc gcc gcc gag gag gag gac				1251
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp				
400		405	410	
tgg gac tac gcc ccc ctg gtg ctg gcc ccc gac gac cgc agc tac aag				1299
Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys				
415		420	425	
agc cag tac ctg aac aac ggc ccc cag cgc atc ggc cgc aag tac aag				1347
Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys				
430		435	440	
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Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu				
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Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu				
460		465	470	475
gtg ggc gac acc ctg ctg atc atc ttc aag aac cag gcc agc cgc ccc				1491
Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro				
480		485	490	
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Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser				
495		500	505	
cgc cgc ctg ccc aag ggc gtg aag cac ctg aag gac ttc ccc atc ctg				1587
Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu				
510		515	520	
ccc ggc gag atc ttc aag tac aag tgg acc gtg acc gtg gag gac ggc				1635
Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly				
525		530	535	

ccc acc aag agc gac ccc cgc tgc ctg acc cgc tac tac agc agc ttc Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe 540 545 550 555	1683
gtg aac atg gag cgc gac ctg gcc agc ggc ctg atc ggc ccc ctg ctg Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu 560 565 570	1731
atc tgc tac aag gag agc gtg gac cag cgc ggc aac cag atc atg agc Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser 575 580 585	1779
gac aag cgc aac gtg atc ctg ttc agc gtg ttc gac gag aac cgc agc Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser 590 595 600	1827
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gtg cag ctg gag gac ccc gag ttc cag gcc agc aac atc atg cac agc Val Gln Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser 620 625 630 635	1923
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gag gtg gcc tac tgg tac atc ctg agc atc ggc gcc cag acc gac ttc Glu Val Ala Tyr Trp Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe 655 660 665	2019
ctg agc gtg ttc ttc agc ggc tac acc ttc aag cac aag atg gtg tac Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr 670 675 680	2067
gag gac acc ctg acc ctg ttc ccc ttc agc ggc gag acc gtg ttc atg Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met 685 690 695	2115
agc atg gag aac ccc ggc ctg tgg atc ctg ggc tgc cac aac agc gac Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp 700 705 710 715	2163
ttc cgc aac cgc ggc atg acc gcc ctg ctg aag gtg agc agc tgc gac Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp 720 725 730	2211
aag aac acc ggc gac tac tac gag gac agc tac gag gac atc agc gcc Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala 735 740 745	2259
tac ctg ctg agc aag aac aac gcc atc gag ccc cgc ctg gag gag atc Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Leu Glu Glu Ile 750 755 760	2307

acc cgc acc acc ctg cag agc gac cag gag gag atc gac tac gac gac Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp 765 770 775	2355
acc atc agc gtg gag atg aag aag gag gac ttc gac atc tac gac gag Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu 780 785 790 795	2403
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atc cgc gcc gag gtg gag gac aac atc atg gtg acc ttc cgc aac cag Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln 880 885 890	2691
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gag acc aag acc tac ttc tgg aag gtg cag cac cac atg gcc ccc acc Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala Pro Thr 925 930 935	2835
aag gac gag ttc gac tgc aag gcc tgg gcc tac ttc agc gac gtg gac Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp Val Asp 940 945 950 955	2883
ctg gag aag gac gtg cac agc ggc ctg atc ggg ccc ctg ctg gtg tgc Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys 960 965 970	2931
cac acc aac acc ctg aac ccc gcc cac ggc cgc cag gtg acc gtg cag His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln 975 980 985	2979
gag ttc gcc ctg ttc ttc acc atc ttc gac gag acc aag agc tgg tac	3027

Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr	
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ttc acc gag aac atg gag cgc aac tgc cgc gcc ccc tgc aac atc cag	3075
Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln	
1005	1010 1015
atg gag gac ccc acc ttc aag gag aac tac cgc ttc cac gcc atc aac	3123
Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn	
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ggc tac atc atg gac acc ctg aaa ggc ctg gtg atg gcc cag gac cag	3171
Gly Tyr Ile Met Asp Thr Leu Lys Gly Leu Val Met Ala Gln Asp Gln	
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cgc atc cgc tgg tac ctg ctg agc atg ggc agc aac gag aac atc cac	3219
Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His	
	1055 1060 1065
agc atc cac ttc agc ggc cac gtg ttc acc gtg cgc aag aag gag gag	3267
Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys Glu Glu	
	1070 1075 1080
tac aag atg gcc ctg tac aac ctg tac ccc ggc gtg ttc gag acc gtg	3315
Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val	
	1085 1090 1095
gag atg ctg ccc agc aag gcc ggc atc tgg cgc gtg gag tgc ctg atc	3363
Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile	
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ggc gag cac ctg cac gcc ggc atg agc acc ctg ttc ctg gtg tac agc	3411
Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser	
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aac aag tgc cag acc ccc ctg ggc atg gcc agc ggc cac atc cgc gac	3459
Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp	
	1135 1140 1145
ttc cag atc acc gcc agc ggc cag tac ggc cag tgg gcc ccc aag ctg	3507
Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu	
	1150 1155 1160
gcc cgc ctg cac tac agc ggc agc atc aac gcc tgg agc acc aag gag	3555
Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu	
	1165 1170 1175
ccc ttc agc tgg atc aag gtg gac ctg ctg gcc ccc atg atc atc cac	3603
Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile Ile His	
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ggc atc aag acc cag ggc gcc cgc cag aac ttc agc agc ctg tac atc	3651
Gly Ile Lys Thr Gln Gly Ala Arg Gln Asn Phe Ser Ser Leu Tyr Ile	
	1200 1205 1210
agc cag ttc atc atc atg tac agc ctg gac ggc aag aag tgg cag acc	3699
Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr	

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Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val			
1230	1235	1240	
gac agc agc ggc atc aag cac aac atc ttc aac ccc ccc atc atc gcc			3795
Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala			
1245	1250	1255	
cgc tac atc cgc ctg cac ccc acc cac tac agc atc cgc agc acc ctg			3843
Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu			
1260	1265	1270	1275
cgc atg gag ctg atg ggc tgc gac ctg aac agc tgc agc atg ccc ctg			3891
Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu			
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Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser			
1295	1300	1305	
tac ttc acc aac atg ttc gcc acc tgg agc ccc agc aag gcc cgc ctg			3987
Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu			
1310	1315	1320	
cac ctg cag ggc cgc agc aac gcc tgg cgc ccc cag gtg aac aac ccc			4035
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro			
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aag gag tgg ctg cag gtg gac ttc cag aag acc atg aag gtg acc ggc			4083
Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly			
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gtg acc acc cag ggc gtg aag agc ctg ctg acc agc atg tac gtg aag			4131
Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys			
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gag ttc ctg atc agc agc agc cag gac ggc cac cag tgg acc ctg ttc			4179
Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe			
1375	1380	1385	
ttc cag aac ggc aag gtg aag gtg ttc cag ggc aac cag gac agc ttc			4227
Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe			
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acc ccc gtg gtg aac agc ctg gac ccc ccc ctg ctg acc cgc tac ctg			4275
Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu			
1405	1410	1415	
cgc atc cac ccc cag agc tgg gtg cac cag atc gcc ctg cgc atg gag			4323
Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu			
1420	1425	1430	1435
gtg ctg ggc tgc gag gcc cag gac ctg tac tagctgccccg ggctacaagc			4373
Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr			
1440	1445		

ttt

4376

&lt;210&gt; 2

&lt;211&gt; 4384

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetically generated insert

&lt;221&gt; CDS

&lt;222&gt; (19)...(4359)

&lt;400&gt; 2

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		1				5						10	

tgc	ctg	ctg	cgc	ttc	tgc	ttc	agc	gcc	acc	cgc	cgc	tac	tac	ctg	ggc	99
Cys	Leu	Leu	Arg	Phe	Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	
			15					20						25		

gcc	gtg	gag	ctg	agc	tgg	gac	tac	atg	cag	agc	gac	ctg	ggc	gag	ctg	147
Ala	Val	Glu	Leu	Ser	Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	
			30				35					40				

ccc	gtg	gac	gcc	cgc	ttc	ccc	ccc	cgc	gtg	ccc	aag	agc	ttc	ccc	ttc	195
Pro	Val	Asp	Ala	Arg	Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	
		45				50					55					

aac	acc	agc	gtg	gtg	tac	aag	aag	acc	ctg	ttc	gtg	gag	ttc	acc	gac	243
Asn	Thr	Ser	Val	Val	Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	
	60				65				70					75		

cac	ctg	ttc	aac	atc	gcc	aag	ccc	cgc	ccc	ccc	tgg	atg	ggc	ctg	ctg	291
His	Leu	Phe	Asn	Ile	Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	
			80					85						90		

ggc	ccc	acc	atc	cag	gcc	gag	gtg	tac	gac	acc	gtg	gtg	atc	acc	ctg	339
Gly	Pro	Thr	Ile	Gln	Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	
			95				100						105			

aag	aac	atg	gcc	agc	cac	ccc	gtg	agc	ctg	cac	gcc	gtg	ggc	gtg	agc	387
Lys	Asn	Met	Ala	Ser	His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	
		110					115					120				

tac	tgg	aag	gcc	agc	gag	ggc	gcc	gag	tac	gac	gac	cag	acc	agc	cag	435
Tyr	Trp	Lys	Ala	Ser	Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	
	125					130				135						

cgc	gag	aag	gag	gac	gac	aag	gtg	ttc	ccc	ggc	ggc	agc	cac	acc	tac	483
Arg	Glu	Lys	Glu	Asp	Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	
140					145					150					155	

gtg	tgg	cag	gtg	ctg	aag	gag	aac	ggc	ccc	atg	gcc	agc	gac	ccc	ctg	531
Val	Trp	Gln	Val	Leu	Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	



160	165	170	
tgc ctg acc tac agc tac ctg agc cac gtg gac ctg gtg aag gac ctg			579
Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu			
175	180	185	
aac agc ggc ctg atc ggc gcc ctg ctg gtg tgc cgc gag ggc agc ctg			627
Asn Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu			
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gcc aag gag aag acc cag acc ctg cac aag ttc atc ctg ctg ttc gcc			675
Ala Lys Glu Lys Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala			
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gtg ttc gac gag ggc aag agc tgg cac agc gag acc aag aac agc ctg			723
Val Phe Asp Glu Gly Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu			
220	225	230	235
atg cag gac cgc gac gcc gcc agc gcc cgc gcc tgg ccc aag atg cac			771
Met Gln Asp Arg Asp Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His			
240	245	250	
acc gtg aac ggc tac gtg aac cgc agc ctg ccc ggc ctg atc ggc tgc			819
Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys			
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cac cgc aag agc gtg tac tgg cac gtg atc ggc atg ggc acc acc ccc			867
His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro			
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gag gtg cac agc atc ttc ctg gag ggc cac acc ttc ctg gtg cgc aac			915
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn			
285	290	295	
cac cgc cag gcc agc ctg gag atc agc ccc atc acc ttc ctg acc gcc			963
His Arg Gln Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala			
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cag acc ctg ctg atg gac ctg ggc cag ttc ctg ctg ttc tgc cac atc			1011
Gln Thr Leu Leu Met Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile			
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agc agc cac cag cac gac ggc atg gag gcc tac gtg aag gtg gac agc			1059
Ser Ser His Gln His Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser			
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tgc ccc gag gag ccc cag ctg cgc atg aag aac aac gag gag gcc gag			1107
Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu			
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gac tac gac gac gac ctg acc gac agc gag atg gac gtg gtg cgc ttc			1155
Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe			
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gac gac gac aac agc ccc agc ttc atc cag atc cgc agc gtg gcc aag			1203
Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys			
380	385	390	395

aag cag ggg aag acc tgg gtg cac tac atc gcc gcc gag gag gag gac	1251
Lys Gln Gly Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp	
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Trp Asp Tyr Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys	
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Ser Gln Tyr Leu Asn Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys	
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Lys Val Arg Phe Met Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu	
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gcc atc cag cac gag agc ggc atc ctg ggc ccc ctg ctg tac ggc gag	1443
Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu	
460 465 470 475	
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Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro	
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Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser	
495 500 505	
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Arg Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu	
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Pro Gly Glu Ile Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly	
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ccc acc aag agc gac ccc cgc tgc ctg acc cgc tac tac agc agc ttc	1683
Pro Thr Lys Ser Asp Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe	
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Val Asn Met Glu Arg Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu	
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Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser	
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Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser	
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Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly	
605 610 615	

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atc aac ggc tac gtg ttc gac agc ctg cag ctg agc gtg tgc ctg cac Ile Asn Gly Tyr Val Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His 640 645 650	1971
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ctg agc gtg ttc ttc agc ggc tac acc ttc aag cac aag atg gtg tac Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr 670 675 680	2067
gag gac acc ctg acc ctg ttc ccc ttc agc ggc gag acc gtg ttc atg Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met 685 690 695	2115
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ttc cgc aac cgc ggc atg acc gcc ctg ctg aag gtg agc agc tgc gac Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp 720 725 730	2211
aag aac acc ggc gac tac tac gag gac agc tac gag gac atc agc gcc Lys Asn Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala 735 740 745	2259
tac ctg ctg agc aag aac aac gcc atc gag ccc cgc agg cgc agg cgc Tyr Leu Leu Ser Lys Asn Asn Ala Ile Glu Pro Arg Arg Arg Arg Arg 750 755 760	2307
gag atc acc cgc acc acc ctg cag agc gac cag gag gag atc gac tac Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr 765 770 775	2355
gac gac acc atc agc gtg gag atg aag aag gag gac ttc gac atc tac Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp Ile Tyr 780 785 790 795	2403
gac gag gac gag aac cag agc ccc cgc agc ttc cag aag aag acc cgc Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys Thr Arg 800 805 810	2451
cac tac ttc atc gcc gcc gtg gag cgc ctg tgg gac tac ggc atg agc His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly Met Ser 815 820 825	2499
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Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr	
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Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly	
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Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg	
880 885 890	
aac cag gcc agc cgc ccc tac agc ttc tac agc agc ctg atc agc tac	2739
Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr	
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Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe Val Lys	
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Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His Met Ala	
925 930 935	
ccc acc aag gac gag ttc gac tgc aag gcc tgg gcc tac ttc agc gac	2883
Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe Ser Asp	
940 945 950 955	
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Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu	
960 965 970	
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Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr	
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Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser	
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Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn	
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atc cag atg gag gac ccc acc ttc aag gag aac tac cgc ttc cac gcc	3123
Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His Ala	
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Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met Ala Gln	
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Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn Glu Asn	
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Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys Lys	

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acc gtg gag atg ctg ccc agc aag gcc ggc atc tgg cgc gtg gag tgc Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys 1100	1105	1110 1115	3363
ctg atc ggc gag cac ctg cac gcc ggc atg agc acc ctg ttc ctg gtg Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val 1120	1125	1130	3411
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cgc gac ttc cag atc acc gcc agc ggc cag tac ggc cag tgg gcc ccc Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp Ala Pro 1150	1155	1160	3507
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cag acc tac cgc ggc aac agc acc ggc acc ctg atg gtg ttc ttc ggc Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly 1230	1235	1240	3747
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ccc ctg ggc atg gag agc aag gcc atc agc gac gcc cag atc acc gcc Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala 1295	1300	1305	3939

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 Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala  
           1310                          1315                          1320

cgc ctg cac ctg cag ggc cgc agc aac gcc tgg cgc ccc cag gtg aac 4035  
 Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn  
           1325                          1330                          1335

aac ccc aag gag tgg ctg cag gtg gac ttc cag aag acc atg aag gtg 4083  
 Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val  
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acc ggc gtg acc acc cag ggc gtg aag agc ctg ctg acc agc atg tac 4131  
 Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr  
                           1360                          1365                          1370

gtg aag gag ttc ctg atc agc agc agc cag gac ggc cac cag tgg acc 4179  
 Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr  
                           1375                          1380                          1385

ctg ttc ttc cag aac ggc aag gtg aag gtg ttc cag ggc aac cag gac 4227  
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                           1390                          1395                          1400

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 Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg  
           1405                          1410                          1415

tac ctg cgc atc cac ccc cag agc tgg gtg cac cag atc gcc ctg cgc 4323  
 Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg  
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atg gag gtg ctg ggc tgc gag gcc cag gac ctg tac tagctgccccg 4369  
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 Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg  
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 Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val  
   50                          55                          60  
 Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile

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Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln
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Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser
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His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser
		115					120					125			
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp
	130					135					140				
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu
145					150					155					160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser
			165						170					175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile
			180					185					190		
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr
	195						200					205			
Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly
	210					215					220				
Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp
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Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr
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Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val
		260					265						270		
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile
	275					280						285			
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser
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Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met
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Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His
			325					330					335		
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Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp
	355					360						365			
Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser
	370					375					380				
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	His	Pro	Lys	Thr
385				390						395					400
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro
			405						410					415	
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn
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Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met
	435					440						445			
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu
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Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu
465				470					475						480
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His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys
	500						505						510		
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe
	515					520						525			

Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp	
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Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg	
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Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val	
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Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu	
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Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val	
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Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp	
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Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe	
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Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr	
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Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly	
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Asn	Asn	Ala	Ile	Glu	Pro	Arg	Leu	Glu	Glu	Ile	Thr	Arg	Thr	Thr	Leu	
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Gln	Ser	Asp	Gln	Glu	Glu	Ile	Asp	Tyr	Asp	Asp	Thr	Ile	Ser	Val	Glu	
770						775					780					
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785					790				795						800	
Pro	Arg	Ser	Phe	Gln	Lys	Lys	Thr	Arg	His	Tyr	Phe	Ile	Ala	Ala	Val	
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Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	Leu	Arg	
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Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	Val	Phe	
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Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	Gly	Glu	
850						855					860					
Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	Glu	Val	
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Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	
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Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	Gln	Gly	
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Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	Thr	Tyr	
		915					920					925				
Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	Phe	Asp	
930						935					940					
Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	Asp	Val	
945					950					955					960	
His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	Thr	Leu	
				965					970					975		
Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	Leu	Phe	



	980		985		990
Phe Thr Ile	Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met				
995		1000		1005	
Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr					
1010		1015		1020	
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp					
1025		1030		1035	1040
Thr Leu Lys Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr					
	1045		1050		1055
Leu Leu Ser Met Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser					
	1060		1065		1070
Gly His Val Phe Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu					
1075		1080		1085	
Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser					
1090		1095		1100	
Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His					
1105		1110		1115	1120
Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr					
	1125		1130		1135
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala					
	1140		1145		1150
Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr					
	1155		1160		1165
Ser Gly Ser Ile Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile					
	1170		1175		1180
Lys Val Asp Leu Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln					
1185		1190		1195	1200
Gly Ala Arg Gln Asn Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile					
	1205		1210		1215
Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser					
	1220		1225		1230
Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile					
	1235		1240		1245
Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu					
	1250		1255		1260
His Pro Thr His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met					
1265		1270		1275	1280
Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys					
	1285		1290		1295
Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met					
	1300		1305		1310
Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg					
	1315		1320		1325
Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln					
	1330		1335		1340
Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly					
1345		1350		1355	1360
Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser					
	1365		1370		1375
Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys					
	1380		1385		1390
Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn					
	1395		1400		1405
Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln					
	1410		1415		1420
Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu					
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Ala Gln Asp Leu Tyr  
1445

<210> 4

<211> 1447

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

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Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser	20	25	30	
Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	35	40	45	
Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	50	55	60	
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile	65	70	75	80
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln	85	90	95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser	100	105	110	
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser	115	120	125	
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	130	135	140	
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	145	150	155	160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	165	170	175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	180	185	190	
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	195	200	205	
Gln	Thr	Leu	His	Lys	Phe	Ile	Leu	Leu	Phe	Ala	Val	Phe	Asp	Glu	Gly	210	215	220	
Lys	Ser	Trp	His	Ser	Glu	Thr	Lys	Asn	Ser	Leu	Met	Gln	Asp	Arg	Asp	225	230	235	240
Ala	Ala	Ser	Ala	Arg	Ala	Trp	Pro	Lys	Met	His	Thr	Val	Asn	Gly	Tyr	245	250	255	
Val	Asn	Arg	Ser	Leu	Pro	Gly	Leu	Ile	Gly	Cys	His	Arg	Lys	Ser	Val	260	265	270	
Tyr	Trp	His	Val	Ile	Gly	Met	Gly	Thr	Thr	Pro	Glu	Val	His	Ser	Ile	275	280	285	
Phe	Leu	Glu	Gly	His	Thr	Phe	Leu	Val	Arg	Asn	His	Arg	Gln	Ala	Ser	290	295	300	
Leu	Glu	Ile	Ser	Pro	Ile	Thr	Phe	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Met	305	310	315	320
Asp	Leu	Gly	Gln	Phe	Leu	Leu	Phe	Cys	His	Ile	Ser	Ser	His	Gln	His	325	330	335	
Asp	Gly	Met	Glu	Ala	Tyr	Val	Lys	Val	Asp	Ser	Cys	Pro	Glu	Glu	Pro	340	345	350	
Gln	Leu	Arg	Met	Lys	Asn	Asn	Glu	Glu	Ala	Glu	Asp	Tyr	Asp	Asp	Asp				

Leu	Thr	Asp	Ser	Glu	Met	Asp	Val	Val	Arg	Phe	Asp	Asp	Asp	Asn	Ser
	370					375					380				
Pro	Ser	Phe	Ile	Gln	Ile	Arg	Ser	Val	Ala	Lys	Lys	Gln	Gly	Lys	Thr
385					390					395					400
Trp	Val	His	Tyr	Ile	Ala	Ala	Glu	Glu	Glu	Asp	Trp	Asp	Tyr	Ala	Pro
				405					410					415	
Leu	Val	Leu	Ala	Pro	Asp	Asp	Arg	Ser	Tyr	Lys	Ser	Gln	Tyr	Leu	Asn
			420					425					430		
Asn	Gly	Pro	Gln	Arg	Ile	Gly	Arg	Lys	Tyr	Lys	Lys	Val	Arg	Phe	Met
		435					440					445			
Ala	Tyr	Thr	Asp	Glu	Thr	Phe	Lys	Thr	Arg	Glu	Ala	Ile	Gln	His	Glu
	450					455					460				
Ser	Gly	Ile	Leu	Gly	Pro	Leu	Leu	Tyr	Gly	Glu	Val	Gly	Asp	Thr	Leu
465					470					475					480
Leu	Ile	Ile	Phe	Lys	Asn	Gln	Ala	Ser	Arg	Pro	Tyr	Asn	Ile	Tyr	Pro
				485					490					495	
His	Gly	Ile	Thr	Asp	Val	Arg	Pro	Leu	Tyr	Ser	Arg	Arg	Leu	Pro	Lys
			500					505					510		
Gly	Val	Lys	His	Leu	Lys	Asp	Phe	Pro	Ile	Leu	Pro	Gly	Glu	Ile	Phe
		515					520					525			
Lys	Tyr	Lys	Trp	Thr	Val	Thr	Val	Glu	Asp	Gly	Pro	Thr	Lys	Ser	Asp
	530					535					540				
Pro	Arg	Cys	Leu	Thr	Arg	Tyr	Tyr	Ser	Ser	Phe	Val	Asn	Met	Glu	Arg
545					550					555					560
Asp	Leu	Ala	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Ile	Cys	Tyr	Lys	Glu
				565					570					575	
Ser	Val	Asp	Gln	Arg	Gly	Asn	Gln	Ile	Met	Ser	Asp	Lys	Arg	Asn	Val
			580					585					590		
Ile	Leu	Phe	Ser	Val	Phe	Asp	Glu	Asn	Arg	Ser	Trp	Tyr	Leu	Thr	Glu
		595					600					605			
Asn	Ile	Gln	Arg	Phe	Leu	Pro	Asn	Pro	Ala	Gly	Val	Gln	Leu	Glu	Asp
	610					615					620				
Pro	Glu	Phe	Gln	Ala	Ser	Asn	Ile	Met	His	Ser	Ile	Asn	Gly	Tyr	Val
625					630					635					640
Phe	Asp	Ser	Leu	Gln	Leu	Ser	Val	Cys	Leu	His	Glu	Val	Ala	Tyr	Trp
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Tyr	Ile	Leu	Ser	Ile	Gly	Ala	Gln	Thr	Asp	Phe	Leu	Ser	Val	Phe	Phe
			660					665					670		
Ser	Gly	Tyr	Thr	Phe	Lys	His	Lys	Met	Val	Tyr	Glu	Asp	Thr	Leu	Thr
		675					680					685			
Leu	Phe	Pro	Phe	Ser	Gly	Glu	Thr	Val	Phe	Met	Ser	Met	Glu	Asn	Pro
	690					695					700				
Gly	Leu	Trp	Ile	Leu	Gly	Cys	His	Asn	Ser	Asp	Phe	Arg	Asn	Arg	Gly
705					710		</								

Ala	Val	Glu	Arg	Leu	Trp	Asp	Tyr	Gly	Met	Ser	Ser	Ser	Pro	His	Val	820	825	830
Leu	Arg	Asn	Arg	Ala	Gln	Ser	Gly	Ser	Val	Pro	Gln	Phe	Lys	Lys	Val	835	840	845
Val	Phe	Gln	Glu	Phe	Thr	Asp	Gly	Ser	Phe	Thr	Gln	Pro	Leu	Tyr	Arg	850	855	860
Gly	Glu	Leu	Asn	Glu	His	Leu	Gly	Leu	Leu	Gly	Pro	Tyr	Ile	Arg	Ala	865	870	875
Glu	Val	Glu	Asp	Asn	Ile	Met	Val	Thr	Phe	Arg	Asn	Gln	Ala	Ser	Arg	885	890	895
Pro	Tyr	Ser	Phe	Tyr	Ser	Ser	Leu	Ile	Ser	Tyr	Glu	Glu	Asp	Gln	Arg	900	905	910
Gln	Gly	Ala	Glu	Pro	Arg	Lys	Asn	Phe	Val	Lys	Pro	Asn	Glu	Thr	Lys	915	920	925
Thr	Tyr	Phe	Trp	Lys	Val	Gln	His	His	Met	Ala	Pro	Thr	Lys	Asp	Glu	930	935	940
Phe	Asp	Cys	Lys	Ala	Trp	Ala	Tyr	Phe	Ser	Asp	Val	Asp	Leu	Glu	Lys	945	950	955
Asp	Val	His	Ser	Gly	Leu	Ile	Gly	Pro	Leu	Leu	Val	Cys	His	Thr	Asn	965	970	975
Thr	Leu	Asn	Pro	Ala	His	Gly	Arg	Gln	Val	Thr	Val	Gln	Glu	Phe	Ala	980	985	990
Leu	Phe	Phe	Thr	Ile	Phe	Asp	Glu	Thr	Lys	Ser	Trp	Tyr	Phe	Thr	Glu	995	1000	1005
Asn	Met	Glu	Arg	Asn	Cys	Arg	Ala	Pro	Cys	Asn	Ile	Gln	Met	Glu	Asp	1010	1015	1020
Pro	Thr	Phe	Lys	Glu	Asn	Tyr	Arg	Phe	His	Ala	Ile	Asn	Gly	Tyr	Ile	1025	1030	1035
Met	Asp	Thr	Leu	Pro	Gly	Leu	Val	Met	Ala	Gln	Asp	Gln	Arg	Ile	Arg	1045	1050	1055
Trp	Tyr	Leu	Leu	Ser	Met	Gly	Ser	Asn	Glu	Asn	Ile	His	Ser	Ile	His	1060	1065	1070
Phe	Ser	Gly	His	Val	Phe	Thr	Val	Arg	Lys	Lys	Glu	Glu	Tyr	Lys	Met	1075	1080	1085
Ala	Leu	Tyr	Asn	Leu	Tyr	Pro	Gly	Val	Phe	Glu	Thr	Val	Glu	Met	Leu	1090	1095	1100
Pro	Ser	Lys	Ala	Gly	Ile	Trp	Arg	Val	Glu	Cys	Leu	Ile	Gly	Glu	His	1105	1110	1115
Leu	His	Ala	Gly	Met	Ser	Thr	Leu	Phe	Leu	Val	Tyr	Ser	Asn	Lys	Cys	1125	1130	1135
Gln	Thr	Pro	Leu	Gly	Met	Ala	Ser	Gly	His	Ile	Arg	Asp	Phe	Gln	Ile	1140	1145	1150
Thr	Ala	Ser	Gly	Gln	Tyr	Gly	Gln	Trp	Ala	Pro	Lys	Leu	Ala	Arg	Leu	1155	1160	1165
His	Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser	1170	1175	1180
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile	Lys	1185	1190	1195
Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser	Gln	Phe	1205	1210	1215
Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr	Tyr	Arg	Gly	1220	1225	1230
Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn	Val	Asp	Ser	Ser	1235	1240	1245
Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile	Ile	Ala	Arg	Tyr	Ile	1250	1255	1260
Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg	Ser	Thr	Leu	Arg	Met	Glu			

1265                      1270                      1275                      1280  
 Leu Met Gly Cys Asp Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu  
                                  1285                      1290                      1295  
 Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr  
                                  1300                      1305                      1310  
 Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu Gln  
                                  1315                      1320                      1325  
 Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu Trp  
                                  1330                      1335                      1340  
 Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr  
 1345                      1350                      1355                      1360  
 Gln Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu  
                                  1365                      1370                      1375  
 Ile Ser Ser Ser Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn  
                                  1380                      1385                      1390  
 Gly Lys Val Lys Val Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val  
                                  1395                      1400                      1405  
 Val Asn Ser Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His  
                                  1410                      1415                      1420  
 Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly  
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 Cys Glu Ala Gln Asp Leu Tyr  
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16

<210> 6  
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16

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<211> 104

<212> DNA

<213> Homo sapiens

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<210> 9

<211> 88

<212> DNA

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<211> 119

<212> DNA

<213> Homo sapiens

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<210> 11

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<212> DNA

<213> Homo sapiens

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<210> 12

<211> 84

<212> DNA

<213> Homo sapiens

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tgcattgctag cctacgaatt ctac 84

<210> 13

<211> 115

<212> DNA

<213> Homo sapiens

<400> 13

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<210> 14  
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<212> DNA  
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caaggtgttc cccggcgga gccacaccta cgtgtggcag gtg 103

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cacgtgctac aagctttac 79

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tc 122

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 <213> Homo sapiens

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 <212> DNA  
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<210> 23  
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 ggagggccac accttcctgg tgcgcaacca ccgcccaggc 99

<210> 26  
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<212> DNA  
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<210> 27  
 <211> 101  
 <212> DNA  
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 aagaacaacg aggaggccga ggactacgac gacgacctga c 101

<210> 28  
 <211> 84  
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 ctctacggat cctacaagct ttac 84

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 <211> 109  
 <212> DNA  
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<210> 30  
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<400> 31  
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<400> 32  
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<210> 33  
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 ag 122

<210> 34  
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 <212> DNA  
 <213> Homo sapiens

<400> 34  
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<210> 35  
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<400> 35  
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<210> 36  
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 <212> DNA  
 <213> Homo sapiens

<400> 36  
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 cccggcgaga tctctacaag ctttac 86

<210> 37  
 <211> 109  
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<400> 37  
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 ttgggcaggc ggccgctgta cagggggcgc acgtcggtga tgccgtggg 109

<210> 38  
 <211> 114  
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<400> 38  
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cctcgccgta cagcaggggg cccaggatgc cgctctcgtg ctggatggcc tcgc 114

<210> 39  
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 <213> Homo sapiens

<400> 39  
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<210> 40  
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 <212> DNA  
 <213> Homo sapiens

<400> 40  
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 gtgcttcttg gccacgctgc ggatccctac gaattctac 99

<210> 41  
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 <212> DNA  
 <213> Homo sapiens

<400> 41  
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 aagagcgacc cccgctgcct gaccgctac tacagcagct tc 102

<210> 42  
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<400> 42  
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 gagagcgtgg accagcgcgg caaccagatc atgagcgaca agc 103

<210> 43  
 <211> 61  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
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 c 61

<210> 44  
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 <212> DNA  
 <213> Homo sapiens

<400> 44  
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 cgcttgctgc tcatgatctg gttgccg 87

<210> 45  
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 <212> DNA  
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<210> 46  
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 <213> Homo sapiens

<400> 46  
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 gatctctacg aattctac 78

<210> 47  
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 <212> DNA  
 <213> Homo sapiens

<400> 47  
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 <213> Homo sapiens

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<210> 49  
 <211> 95  
 <212> DNA  
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<400> 49  
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 gagaaccccg gcctgtggat ccctacaagc ttac 95

<210> 50  
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 <212> DNA  
 <213> Homo sapiens

<400> 50  
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<210> 51  
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<212> DNA

<213> Homo sapiens

<400> 51

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catg	124

<210> 52

<211> 98

<212> DNA

<213> Homo sapiens

<400> 52

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<210> 53

<211> 111

<212> DNA

<213> Homo sapiens

<400> 53

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<210> 54

<211> 102

<212> DNA

<213> Homo sapiens

<400> 54

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<210> 55

<211> 105

<212> DNA

<213> Homo sapiens

<400> 55

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gacgaggacg agaaccagag cccccgcagc ttccagaaga agacc	105

<210> 56

<211> 79

<212> DNA

<213> Homo sapiens

<400> 56

cgccactact tcatcgccgc cgtggagcgc ctgtgggact acggcatgag cagcagcccc	60
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<210> 57

<211> 101

<212> DNA

<213> Homo sapiens

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<210> 58  
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 <212> DNA  
 <213> Homo sapiens

<400> 58  
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<210> 59  
 <211> 108  
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<400> 59  
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 ctgatgtcct cgtagctgtc ctcgtagtag tcgcgggtgt tcttgctg 108

<210> 60  
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 <212> DNA  
 <213> Homo sapiens

<400> 60  
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 cccaggatcc ctacgaattc tac 83

<210> 61  
 <211> 115  
 <212> DNA  
 <213> Homo sapiens

<400> 61  
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 gaaggtgggtg ttccaggagt tcaccgacgg cagcttcacc cagccctgt accgc 115

<210> 62  
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 <212> DNA  
 <213> Homo sapiens

<400> 62  
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 aacatcatgg tgaccgtgca ggagttcgcc ctgttcttca ccatcttcga c 111

<210> 63  
 <211> 106  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
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atccagatgg aggacccac cttcaaggag aactaccgct tccacg 106

<210> 64  
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 <212> DNA  
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<400> 64  
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 tccgctggta ccctacaagc ttac 85

<210> 65  
 <211> 115  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
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 gtgtccatga tgtagccgtt gatggcgtgg aagcggtagt tctccttgaa ggtgg 115

<210> 66  
 <211> 99  
 <212> DNA  
 <213> Homo sapiens

<400> 66  
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 accagctctt ggtctcgtcg aagatggtga agaacaggg 99

<210> 67  
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 <212> DNA  
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<400> 67  
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 gcaggcccag gtgctcgttc agctcgccgc ggtacagggg ctgggtgaag 110

<210> 68  
 <211> 93  
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 <213> Homo sapiens

<400> 68  
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 gcgcggttgc gcagcacgtg ctacgaattc tac 93

<210> 69  
 <211> 116  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
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<210> 70

<211> 120  
 <212> DNA  
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<400> 70  
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 aaggacgagt tcgactgcaa ggcctggggcc tacttcagcg acgtggacct ggagaaggac 120

<210> 71  
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 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 cacggcggcc aggtgaccct acaagcttta c 91

<210> 72  
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 <212> DNA  
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<400> 72  
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<210> 73  
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 <212> DNA  
 <213> Homo sapiens

<400> 73  
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 c 121

<210> 74  
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<400> 74  
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 cctggttgcg gaaggtcacc ctacgaattc tac 93

<210> 75  
 <211> 120  
 <212> DNA  
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<400> 75  
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 ttcagcggcc acgtgttcac cgtgcgcaag aaggaggagt acaagatggc cctgtacaac 120

<210> 76  
 <211> 122  
 <212> DNA



<213> Homo sapiens

<400> 76

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gtggagtgcc tgatcggcga gcacctgcac gccggcatga gcacctgtt cctggtgtac	120
ag	122

<210> 77

<211> 102

<212> DNA

<213> Homo sapiens

<400> 77

caacaagtgc cagaccccc tgggcatggc cagcggccac atccggcact tccagatcac	60
cgccagcggc cagtacggcc agtgggcccc tacaagcttt ac	102

<210> 78

<211> 123

<212> DNA

<213> Homo sapiens

<400> 78

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atgtggccgc tggccatgcc caggggggtc tggcacttgt tgctgtacac caggaacagg	120
gtg	123

<210> 79

<211> 125

<212> DNA

<213> Homo sapiens

<400> 79

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ctgggcagca tctccacggg ctggaacacg cgggggtaca ggttgtacag ggccatcttg	120
tactc	125

<210> 80

<211> 96

<212> DNA

<213> Homo sapiens

<400> 80

ctccttcttg cgcacgggtga acacgtggcc gctgaagtgg atgctgtgga tgttctcggt	60
gctgcccattg ctgagcagg accctacgaa ttctac	96

<210> 81

<211> 120

<212> DNA

<213> Homo sapiens

<400> 81

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<210> 82

<211> 116

<212> DNA

<213> Homo sapiens

<400> 82

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atcatcatgt acagcctgga cggcaagaag tggcagacct accgcggcaa cagcac 116

<210> 83

<211> 86

<212> DNA

<213> Homo sapiens

<400> 83

cggcaccctg atggtgttct tcggcaacgt ggacagcagc ggcatcaagc acaacatctt 60  
caaccccccc gggctacaag ctttac 86

<210> 84

<211> 110

<212> DNA

<213> Homo sapiens

<400> 84

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tgccgaagaa caccatcagg gtgccggtgc tgttgccgcg gtaggtctgc 110

<210> 85

<211> 113

<212> DNA

<213> Homo sapiens

<400> 85

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ttctggcggg cgccctgggt cttgatgccg tggatgatca tggggggccag cag 113

<210> 86

<211> 99

<212> DNA

<213> Homo sapiens

<400> 86

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<210> 87

<211> 122

<212> DNA

<213> Homo sapiens

<400> 87

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<210> 88

<211> 112

<212> DNA

<213> Homo sapiens

<400> 88  
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<400> 89  
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 gaccatgaag gtgaccctac aagctttac 89

<210> 90  
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<210> 91  
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 <212> DNA  
 <213> Homo sapiens

<400> 91  
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<210> 92  
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<400> 92  
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<210> 93  
 <211> 122  
 <212> DNA  
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<400> 93  
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 tc 122

<210> 94  
 <211> 104  
 <212> DNA  
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<400> 94  
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agcctggacc cccccctgct gacccgctac ctgcgcatcc accc 104

<210> 95  
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<400> 95  
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 cctgtactag ctgcccgggc tacaagcttt ac 92

<210> 96  
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 <212> DNA  
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<400> 96  
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 <212> DNA  
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 cttcaccttg ccgttctgga agaacagggt ccactggttg 100

<210> 98  
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<210> 99  
 <211> 140  
 <212> DNA  
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 acatcagcgc ctacctgctg 140

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 <211> 57  
 <212> DNA  
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<400> 100  
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<210> 101

<211> 58  
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 <213> Homo sapiens

<400> 101  
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<210> 102  
 <211> 79  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
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 tggcgcgggt gatctcgcg 79

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<210> 104  
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<220>  
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<400> 105  
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 ctacatgcag agcgacctgg gcgagctgcc cgtggacgcc cgcttcccc cccgcgtgcc 180  
 caagagcttc cccttcaaca ccagcgtggt gtacaagaag accctgttcg tggagtacac 240  
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 caagctttac 310

<210> 106  
 <211> 297  
 <212> DNA  
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<220>  
 <223> synthetically generated construct

<400> 106  
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 ccagcgaggg cgccgagtac gacgaccaga ccagccagcg cgagaaggag gacgacaagg 180  
 tgttccccgg cggcagccac acctacgtgt ggcaggtgct gaaggagaac ggccccatgg 240  
 ccagcgaccc cctgtgcctg acctacagct acctgagcca cgtgctacaa gctttac 297

<210> 107  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 107  
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 tcctgctgtt cgccgtgttc gacgagggca agagctggca cagcgagacc aagaacagcc 180  
 tgatgcagga ccgcgacgcc gccagcgccc gcgcctggcc caagatgcac accgtgaacg 240  
 gctacgtgaa ccgcagcctg cccggcctga tcggctgcca ccgcaagagc gtgtactggc 300  
 acgtgctaca agctttac 318

<210> 108  
 <211> 384  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 108  
 gtagaattcg tagcacgtga tcggcatggg caccaccccc gaggtgcaca gcatttctct 60  
 ggagggccac accttctctg tgcgcaacca ccgccaggcc agcctggaga tcagcccat 120  
 caccttctctg accgcccaga cctgctgat ggacctgggc cagttctctgc tgttctgcca 180  
 catcagcagc caccagcacg acggcatgga ggcctacgtg aaggtggaca gctgcccga 240  
 ggagccccag ctgcgcatga agaacaacga ggaggccgag gactacgacg acgacctgac 300  
 cgacagcgag atggacgtgg tgcgcttcga cgacgacaac agccccagct tcattccagat 360  
 ctctacggat cctacaagct ttac 384

<210> 109  
 <211> 443  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 109  
 gtagaattcg tagggatccg cagcgtggcc aagaagcacc ccaagacctg ggtgcactac 60  
 atcggcgccg aggaggagga ctgggactac gcccccttg tgctggcccc cgacgaccgc 120  
 agctacaaga gccagtacct gaacaacggc cccagcgca tcggccgcaa gtacaagaag 180  
 gtgcgcttca tggcctacac cgacgagacc ttcaagaccc gcgaggccat ccagcacgag 240  
 agcggcatcc tgggccccct gctgtacggc gaggtgggag acacctgct gatcatcttc 300  
 aagaaccagg ccagccgccc ctacaacatc tccccacg gcataccga cgtgcgcccc 360  
 ctgtacagcc gccgcctgcc caaggcgctg aagcacctga aggacttccc catcctgcc 420  
 ggcgagatct ctacaagctt tac 443

<210> 110  
 <211> 266  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 110  
 gtaaagcttg tagggtacca gctgcggttc tcgtcgaaca cgctgaacag gatcacgttg 60  
 cgcttgctgc tcatgatctg gttgccgcgc tgggccacgc tctccttgta gcagatcagc 120  
 agggggccga tcaggccgct ggccaggctc cgctccatgt tcacgaagct gctgtagtag 180  
 cgggtcaggc agcgggggtc gctcttggtg gggccgtcct ccacggtcac ggtccacttg 240  
 tacttgaaga tctctacgaa ttctac 266

<210> 111  
 <211> 341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 111  
 gtagaattcg tagggtacct gaccgagaac atccagcgct tctgccc aa cccgcgcggc 60  
 gtgcagcttg aggaccccga gttccaggcc agcaacatca tgcacagcat caacggctac 120  
 gtgttcgaca gcttgcagct gagcgtgtgc ctgcacgagg tggcctactg gtacatcctg 180  
 agcatcggcg ccagaccga cttcctgagc gtgttcttca ggggtacac cttcaagcac 240  
 aagatgggtg acgaggacac cctgacctg ttcccttca ggggcgagac cgtgttcatg 300  
 agcatggaga accccggcct gtggatccct acaagcttta c 341

<210> 112  
 <211> 397  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 112  
 gtagaattcg tagggatcct gggctgccac aacagcgact tccgaaccg cggcatgacc 60  
 gccctgctga aggtgagcag ctgcgacaag aacaccggcg actactacga ggacagctac 120  
 gaggacatca gcgcctacct gctgagcaag aacaacgcca tcgagccccg cctggaggag 180  
 atcacccgca ccacctgca gagcgaccag gaggagatcg actacgacga caccatcagc 240  
 gtggagatga agaaggagga cttcgacatc tacgacgagg acgagaacca gagccccgc 300  
 agcttccaga agaagaccg ccactacttc atcgccgcg tggagcgct gtgggactac 360  
 ggcatgagca gcagccccca cgtgctacaa gctttac 397

<210> 113  
 <211> 417  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 113  
 gtagaattcg tagcacgtgc tgcgcaaccg cgcccagagc ggcagcgtgc cccagttcaa 60  
 gaaggtggtg ttccaggagt tcaccgacgg cagcttcacc cagcccctgt accgcggcga 120  
 gctgaacgag cacctgggccc tgctgggccc ctacatccgc gccgaggtgg aggacaacat 180  
 catggtgacc gtgcaggagt tcgccctggt cttcaccatc ttcgacgaga ccaagagctg 240  
 gtacttcacc gagaacatgg agcgcaactg ccgcgcccc tgcaacatcc agatggagga 300  
 cccaccttc aaggagaact accgcttcca cgccatcaac ggctacatca tggacaccct 360  
 gcccggcctg gtgatggccc aggaccagcg catccgctgg taccctacaa gctttac 417

<210> 114  
 <211> 327  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 114  
 gtagaattcg tagggtgacc ttccgcaacc aggccagccg cccctacagc ttctacagca 60  
 gcctgatcag ctacgaggag gaccagcgcc agggcgccga gcccgcgaag aacttcgtga 120  
 agcccaacga gaccaagacc tacttctgga aggtgcagca ccacatggcc cccaccaagg 180  
 acgagttcga ctgcaaggcc tgggcctact tcagcgacgt ggacctggag aaggacgtgc 240  
 acagcggcct gatcggcccc ctgctggtgt gccacaccaa caccctgaac cccgcccacg 300  
 gccgccaggt gaccctacaa gctttac 327

<210> 115  
 <211> 344  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 115  
 gtagaattcg tagggtacct gctgagcatg ggcagcaacg agaacatcca cagcatccac 60  
 ttcagcggcc acgtgttcac cgtgcgcaag aaggaggagt acaagatggc cctgtacaac 120  
 ctgtaccccg gcgtgttcga gaccgtggag atgctgcca gcaaggccgg catctggcgc 180  
 gtggagtgcc tgatcggcga gcacctgcac gccggcatga gcacctggt cctggtgtac 240  
 agcaacaagt gccagacccc cctgggcatg gccagcggcc acatccgcga cttccagatc 300  
 accgccagcg gccagtagcg ccagtgggcc cctacaagct ttac 344

<210> 116  
 <211> 322  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 116  
 gtagaattcg taggggcccc caagctggcc cgctgcact acagcggcag catcaacgcc 60  
 tggagcacca aggagccctt cagctggatc aaggtggacc tgctggcccc catgatcacc 120  
 cacggcatca agaccaggc cgcccgcag aagttcagca gcctgtacat cagccagttc 180  
 atcatcatgt acagcctgga cggcaagaag tggcagacct accgcggcaa cagcaccggc 240  
 accctgatgg tgttcttcgg caacgtggac agcagcggca tcaagcaca catcttcaac 300  
 cccccgggc tacaagcttt ac 322



<210> 117  
 <211> 323  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 117  
 gtagaattcg taggatatca tcgcccgcta catccgcctg caccaccacc actacagcat 60  
 ccgcagcacc ctgcgcatgg agctgatggg ctgcgacctg aacagctgca gcatgccct 120  
 gggcatggag agcaaggcca tcagcgacgc ccagatcacc gccagcagct acttcaccaa 180  
 catgttcgcc acctggagcc ccagcaaggc ccgcctgcac ctgcagggcc gcagcaacgc 240  
 ctggcgcccc caggtgaaca accccaagga gtggctgcag gtggacttcc agaagaccat 300  
 gaaggtgacc ctacaagctt tac 323

<210> 118  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 118  
 gtagaattcg tagggtgacc ggcgtgacca ccagggcgt gaagagcctg ctgaccagca 60  
 tgtacgtgaa ggagttcctg atcagcagca gccaggacgg ccaccagtgg accctgttct 120  
 tccagaacgg caaggtgaag gtgttccagg gcaaccagga cagcttcacc cccgtgggtga 180  
 acagcctgga cccccccctg ctgacccgct acctgcgcac ccacccccag agctgggtgc 240  
 accagatcgc cctgcgcgat gaggtgctgg gctgcgaggg ccaggacctg tactagctgc 300  
 ccgggctaca agctttac 318

<210> 119  
 <211> 310  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 119  
 gtaaagcttg taggggcccc gcaggcccat ccaggggggg cggggcttgg cgatgttgaa 60  
 caggtggctg gtgaactcca cgaacagggt cttcttgtag accacgctgg tgttgaaggg 120  
 gaagctcttg ggcacgcggg gggggaagcg ggcgtccacg ggcagctcgc ccaggtcgt 180  
 ctgcatgtag tcccagctca gctccacggc gccaggtag tagcggcggg tggcgctgaa 240  
 gcagaagcgc agcaggcaca ggaagaagca ggtgctcagc tcgatctgca tgctagccta 300  
 cgaattctac 310

<210> 120  
 <211> 297  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 120

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gtaaagcttg tagcacgtgg ctacaggtagc tgtaggtcag gcacagggggg tcgctggcca      60
tgggggccgtt ctcccttcagc acctgccaca cgtaggtgtg gctgccgccg gggaacacct      120
tgtcgctctc ctctctcgcg tggctggtct ggtcgctcgt ctcgccgccg tcgctggcct      180
tccagtagct caccgccacg gcgtgcaggc tcacgggggt gctggccatg ttcttcaggg      240
tgatcaccac ggtgtcgtac acctcggcct ggatggtggg gcccctacga attctac      297

```

<210> 121  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

```

<400> 121
gtaaagcttg tagcacgtgc cagtacacgc tcttgcggtg gcagccgata aggccgggca      60
ggctgcggtt cactagaccg ttacaggtgt gcattctggg ccaggccgag gcgctggcgg      120
cgctcgcggtc ctgcatcagg ctgttcttgg tctcgctgtg ccagctcttg cctcgtcga      180
acacggcgaa cagcaggatg aacttgtgca gggctctgggt cttctccttg gccaggctgc      240
cctcgcgga caccagcagg gcgccgatca ggccgctgtt caggtccttc accagggtcca      300
cgtggctacg aattctac      318

```

<210> 122  
 <211> 384  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

```

<400> 122
gtaaagcttg taggatccgt agagatctgg atgaagctgg ggctgttgtc gtcgtcgaag      60
cgcaccacgt ccatctcgtt gtcggtcagg tcgtcgctgt agtcctcggc ctctcgttg      120
ttcttcatgc gcagctgggg ctctcggggg cagctgtcca ccttcacgta ggccctccatg      180
ccgtcgtgct ggtggctgct gatgtggcag aacagcagga actggcccag gtccatcagc      240
agggctctgg cggtcaggaa ggtgatgggg ctgatctcca ggctggcctg gcggtgggtg      300
cgcaccagga aggtgtggcc ctccaggaag atgctgtgca cctcgggggg ggtgcccatg      360
ccgatcacgt gctacgaatt ctac      384

```

<210> 123  
 <211> 443  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

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<400> 123
gtaaagcttg tagagatctc gccgggcagg atggggaagt ccttcagggt cttcacgccc      60
ttgggcaggc ggcggctgta cagggggcgc acgtcggtga tgccgtgggg gtagatgttg      120
taggggcggc tggcctggtt cttgaagatg atcagcaggg tgctgcccac ctgcgcgtac      180
agcagggggc ccaggatgcc gctctcgtgc tggatggcct cgcgggtctt gaaggtctcg      240
tcggtgtagg ccatgaagcg cacttcttgg tacttgcggc cgatgcgctg ggggcccgtt      300
ttcagggtact ggctcttgta gctgcggtcg tcgggggcca gcaccagggg ggcgtagtcc      360
cagtcctcct cctcggcggc gatgtagtgc acccagggtc tggggtgctt cttggccacg      420
ctgcggatcc ctacgaattc tac      443

```

<210> 124  
 <211> 266  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 124  
 gtagaattcg tagagatctt caagtacaag tggaccgtga ccgtggagga cggccccacc 60  
 aagagcgacc cccgctgcct gacccgctac tacagcagct tcgtgaacat ggagcgcgac 120  
 ctggccagcg gcctgacgag cccctgctg atctgctaca aggagagcgt ggaccagcgc 180  
 ggcaaccaga tcatgagcga caagcgcaac gtgatcctgt tcagcgtggt cgacgagAAC 240  
 cgcagctggt accctacaag ctttac 266

<210> 125  
 <211> 341  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 125  
 gtaaagcttg tagggatcca caggccgggg ttctccatgc tcatgaacac ggtctcgccg 60  
 ctgaagggga acagggtcag ggtgtcctcg tacaccatct tgtgcttgaa ggtgtagccg 120  
 ctgaagaaca cgctcaggaa gtcgggtctgg gcgcccagtc tcaggatgta ccagtaggcc 180  
 acctcgtgca ggcacacgct cagctgcagg ctgtcgaaca cgtagccggt gatgctgtgc 240  
 atgatgttgc tggcctggaa ctcggggtcc tccagctgca cgcgggcggg gttgggcagg 300  
 aagcgtgga tgttctcggt cagggtaccct acgaattcta c 341

<210> 126  
 <211> 397  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 126  
 gtaaagcttg tagcacgtgg gggctgctgc tcatgccgta gtcccacagg cgctccacgg 60  
 cggcgatgaa gtagtggcgg gtcttcttct ggaagctgcg ggggctctgg ttctcgtcct 120  
 cgctcgtagat gtogaagtcc tccttcttca tctccacgct gatgggtgctg tcgtagtcga 180  
 tctcctcctg gtcgctctgc aggggtggtgc gggatgatctc ctccaggcgg ggctcgatgg 240  
 cgttggttctt gtcacagcag taggcgctga tgtcctcgta gctgtcctcg tagtagtcgc 300  
 cgggtgttctt gtcgcagctg ctacacctca gcagggcggg catgccgcgg ttgcggaagt 360  
 cgctgttgtg gcagcccagg atccctacga attctac 397

<210> 127  
 <211> 417  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 127

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gtaaagcttg tagggtacca gcggatgcgc tggctctggg ccatcaccag gccgggcagg      60
gtgtccatga tgtagccgtt gatggcgtgg aagcggtagt tctccttgaa ggtgggggtcc    120
tccatctgga tgttgcaggg ggcgcggcag ttgcgctcca tgttctcggg gaagtaccag    180
ctcttgggtct cgtcgaagat ggtgaagaac agggcgaact cctgcacggg caccatgatg    240
ttgtcctcca cctcggcgcg gatgtagggg ccagcaggc ccagggtgctc gttcagctcg    300
ccgcgggtaca ggggctgggt gaagctgccg tcgggtgaact cctggaacac caccttcttg    360
aactgggggca cgctgccgct ctgggcgcgg ttgcgcagca cgtgctacga attctac      417

```

<210> 128

<211> 327

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 128

```

gtaaagcttg tagggtcacc tggcggccgt gggcgggggt caggggtgttg gtgtggcaca      60
ccagcagggg gccgatcagg ccgctgtgca cgtccttctc cagggtccacg tcgctgaagt    120
aggcccaggc cttgcagtcg aactcgtcct tgggtggggg catgtgggtgc tgcaccttcc    180
agaagtaggt cttgggtctcg ttgggcttca cgaagtctct gcggggctcg gcgccctggc    240
gctgggtcctc ctcgtagctg atcaggctgc tgtagaagct gtaggggcgg ctggcctggt    300
tgcggaaggt caccctacga attctac      327

```

<210> 129

<211> 344

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 129

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gtaaagcttg taggggcccc ctggccgtac tggccgctgg cgggtgatctg gaagtcgcgg      60
atgtggccgc tggccatgcc caggggggtc tggcacttgt tgctgtacac caggaacagg    120
gtgctcatgc cggcgtgcag gtgctcgccg atcaggcact ccacgcgcca gatgccggcc    180
ttgctgggca gcatctccac ggtctcgaac acgccggggg acaggttgta cagggccatc    240
ttgtactcct ccttcttgcg cacggtgaac acgtggccgc tgaagtggat gctgtggatg    300
ttctcgtttg tgcccatgct cagcagggtac cctacgaatt ctac      344

```

<210> 130

<211> 322

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 130

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gtaaagcttg tagcccgggg ggggtgaaga tgttgtgctt gatgccgctg ctgtccacgt      60
tgccgaagaa caccatcagg gtgccggtgc tgttgccgcg gtaggtctgc cacttcttgc    120
cgtccaggct gtacatgatg atgaactggc tgatgtacag gctgctgaac ttctggcggg    180
cgccctgggt cttgatgccg tggatgatca tggggggccag cagggtccacc ttgatccagc    240
tgaagggctc cttgggtgctc caggcggtga tgctgccgct gtagtgcagg cgggccaagt    300
tggggggcccc tacgaattct ac      322

```

<210> 131

<211> 323  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 131  
 gtaaagcttg tagggtcacc ttcattggtct tctggaagtc cacctgcagc cactccttgg 60  
 ggttggtcac ctggggggcgc caggcggttc tgcggccctg cagggtgcagg cgggccttgc 120  
 tggggctcca ggtggcgaac atgttggtga agtagctgct ggcggtgatc tgggcgtcgc 180  
 tgatggcctt gctctccatg ccaggggca tgctgcagct gttcaggctc cagcccatca 240  
 gctccatgcg cagggtgctg cggatgctgt agtgggtggg gtgcaggcgg atgtagcggg 300  
 cgatgatatc ctacgaattc tac 323

<210> 132  
 <211> 318  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 132  
 gtaaagcttg tagcccgggc agctagtaca ggtcctgggc ctgcagccc agcacctcca 60  
 tgcgcagggc gatctggtgc acccagctct gggggtggat gcgcaggtag cgggtcagca 120  
 ggggggggtc caggctgttc accacggggg tgaagctgtc ctgggtgccc tggaacacct 180  
 tcaccttgcc gttctggaag aacagggtcc actggtggcc gtcttggtc ctgctgatca 240  
 ggaactcctt caggtacatg ctggtcagca ggctcttcac gccctgggtg gtcacgcggg 300  
 tcacctacg aattctac 318

<210> 133  
 <211> 255  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 133  
 gtagaattcg gatcctgggc tgccacaaca ggcacttcg caaccgggc atgaccgccc 60  
 tgctgaaggt gagcagctgc gacaagaaca ccggcgacta ctacgaggac agctacgagg 120  
 acatcagcgc ctacctgctg agcaagaaca acgccatcga gcccgagcagg cgcaggcgcg 180  
 agatcacccg caccaccctg cagagcgacc aggaggagat cgactacgac gacaccatca 240  
 gcgtggaagc ttac 255

<210> 134  
 <211> 255  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthetically generated construct

<400> 134  
 gtaaagcttc cacgctgatg gtgtcgtcgt agtcgatctc ctctgggtcg ctctgcaggg 60  
 tgggtgcgggt gatctcgcgc ctgcgcctgc ggggctcgat ggcgttggtc ttgctcagca 120

ggtaggcgct gatgtcctcg tagctgtcct cgtagtagtc gccggtgttc ttgtcgcagc	180
tgctcacctt cagcagggcg gtcatgccgc ggttgccgaa gtcgctgttg tggcagccca	240
ggatccgaat tctac	255

<210> 135

<211> 4

<212> PRT

<213> Homo sapiens

<400> 135

Arg Arg Arg Arg

1

<210> 136

<211> 5

<212> PRT

<213> Homo sapiens

<400> 136

Arg Arg Arg Arg Arg

1

5